

Table S4: Associations recapitulated in non-independent studies. Regions which are significant either by single marker analysis, conditional regression, or a PMR method and which recapitulate a known association to the same disease in a non-independent study that includes data from the WTCCC. The table includes all regions with a VBAY posterior probability > 0.97 , an MCP p-value $< 1 \times 10^{-7}$, or a p-value for any other method $< 1 \times 10^{-6}$.

disease	SNP	chromosome	position	Method										genes	references
				SMA	Conditional	VBAY	Lasso	Adaptive Lasso	2D-MCP	LOG	NEG	1D-MCP	perm-MCP		
CD	rs688532	1q24.3	172,892,951	8.35×10^{-06}	5.53×10^{-06}	0.764	1.15×10^{-05}	1.74×10^{-05}	9.26×10^{-08}	7.83×10^{-06}	1.61×10^{-07}	8.56×10^{-06}	-	Intergenic	[1, 2]
CD	rs1000113	5q33.1	150,240,075	5.99×10^{-07}	5.99×10^{-07}	0.973	3.69×10^{-05}	3.11×10^{-05}	1.49×10^{-10}	1.21×10^{-05}	6.14×10^{-07}	9.02×10^{-06}	-	IRGM	[1, 3, 2, 4]
CD	rs6908425	6p22.3	20,728,730	2.57×10^{-06}	2.57×10^{-06}	0.973	4.54×10^{-08}	1.32×10^{-08}	9.3×10^{-07}	2.69×10^{-07}	4.18×10^{-07}	3.59×10^{-08}	-	CDKAL1	[2]
CD	rs4870943	8q24.13	126,546,388	2.01×10^{-05}	0.864	1.14×10^{-05}	2.24×10^{-05}	9.59×10^{-09}	7.12×10^{-06}	7.73×10^{-06}	3.78×10^{-06}	-	Intergenic	[2]	
CD	rs10883365	10q24.2	101,287,763	5.55×10^{-08}	5.55×10^{-08}	0.99	3.78×10^{-06}	1.87×10^{-06}	1.03×10^{-08}	2.85×10^{-06}	1.57×10^{-06}	4.83×10^{-06}	-	NKX2-3	[1, 3, 2, 4]
CD	rs744166	17q21.2	40,514,200	1.9×10^{-05}	1.78×10^{-05}	0.0246	5.53×10^{-05}	3.58×10^{-05}	9.21×10^{-08}	9.31×10^{-05}	1.84×10^{-01}	2.97×10^{-05}	-	STAT3	[2]
CD	rs16939895	18p11.21	12,821,902	9.2×10^{-09}	1	1	2.44×10^{-08}	8.41×10^{-09}	3.45×10^{-13}	2.32×10^{-08}	1×10^{-09}	2.32×10^{-09}	-	PTPN2	[1, 3, 2]
CD	rs2836754	21q22.2	40,291,739	5.22×10^{-05}	2.66×10^{-05}	0.0487	1.19×10^{-05}	3.31×10^{-05}	5.88×10^{-07}	7×10^{-06}	7.34×10^{-08}	9.66×10^{-07}	-	Intergenic	[1]
T1D	rs17388568	4q27	123,329,361	2.87×10^{-07}	2.87×10^{-07}	-	4.33×10^{-05}	1.54×10^{-05}	-	-	-	-	-	IL2	[5]
T1D	rs7398833	12q24.12	111,786,891	1.36×10^{-07}	1.36×10^{-07}	0.119	1.89×10^{-06}	3.34×10^{-12}	5.74×10^{-14}	7.09×10^{-07}	-	1.63×10^{-07}	-	C12orf30, SH2B3	[6, 5]
T1D	rs12150079	17q12	38,025,416	1.21×10^{-03}	2.83×10^{-05}	0.0153	1×10^{-04}	1.8×10^{-04}	6.32×10^{-10}	2.47×10^{-05}	-	1.91×10^{-04}	-	ORMDL3	[5]

References

- [1] Parkes M, Barrett JC, Prescott NJ, Tremelling M, Anderson Ca, et al. (2007) Sequence variants in the autophagy gene IRGM and multiple other replicating loci contribute to Crohn's disease susceptibility. *Nature Genetics* 39: 830–2.
- [2] Barrett JC, Hansoul S, Nicolae DL, Cho JH, Duerr RH, et al. (2008) Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. *Nature Genetics* 40: 955–62.
- [3] Wellcome Trust Case Control Consortium (2007) Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature* 447: 661–78.
- [4] Franke A, McGovern DPB, Barrett JC, Wang K, Radford-Smith GL, et al. (2010) Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. *Nature Genetics* 42: 1118–25.
- [5] Barrett JC, Clayton DG, Concannon P, Akolkar B, Cooper JD, et al. (2009) Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes. *Nature Genetics* 41: 703–707.
- [6] Cooper JD, Smyth DJ, Smiles AM, Plagnol V, Walker NM, et al. (2008) Meta-analysis of genome-wide association study data identifies additional type 1 diabetes risk loci. *Nature Genetics* 40: 1399–1401.